AMENDMENT TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

What is claimed is:

1. (Previously amended) A method for identification of a pathogenic Gram positive bacterium or a subset of pathogenic Gram positive bacteria from a predetermined group of pathogenic Gram positive bacteria in a clinical sample comprising:

a) providing said clinical sample containing at least partially purified nucleic acid,

b) subjecting said clinical sample to at least one amplification step and at least one detection step in one reaction vessel, said steps comprising:

ba) at least one set of amplification primers capable of amplifying a pre-selected nucleic acid sequence comprising at least 20 nucleotides of the 16S/23S spacer region from a predetermined sub-group of pathogenic Gram positive bacteria to which said pathogenic Gram positive bacterium or subset of pathogenic Gram positive bacteria belongs,

bb) at least one internal control template, and

bc) at least one hybridization reagent capable of detecting said pre-selected nucleic acid sequence from said predetermined sub-group of pathogenic Gram positive bacteria, further comprising:

bca) monitoring hybridization of said hybridization reagent at a pre-selected temperature, said hybridization being indicative for the presence in said clinical sample of at least one species contained in said predetermined sub-group, and

bcb) monitoring temperature dependence of hybridization, said temperature dependence being indicative for the presence of at least the species of said pathogenic Gram positive bacterium or said subset of pathogenic Gram positive bacteria,

wherein said pathogenic Gram positive bacterium or said subset of pathogenic Gram positive bacteria is identified based on the results of the monitoring steps in bca) and bcb).

2. (Previously amended ) The method according to claim 1, wherein said predetermined sub-group is a genus.

3. (Previously amended ) The method according to claim 1, wherein said hybridization reagent comprises two probes complementary to adjacent sequences in said pre-selected nucleic acid sequence, one being labeled by a Fluorescence Resonance Energy Transfer (FRET) donor, and the other being labeled by a FRET acceptor.

4. (Previously amended ) The method according to claim 1, wherein said predetermined group of pathogenic Gram positive bacteria comprises the species *Staphylococcus aureus* and *coagulase-negative staphococci.*

5. (Previously amended ) The method according to claim 1, wherein said predetermined sub-group comprises the species *Staphylococcus aureus, Streptococcus pneumoniae, Enterococcus faecium* and *Enterococcus faecalis.*

6. Cancelled.
7. Cancelled.

8. (Previously amended ) The method according to claim 1, wherein said species are selected from the genera *Staphylococcus, Enterococcus* and *Streptococcus.*

9. (Previously amended ) The method according to claim 1, wherein said species are selected from the genus *Staphylococcus.*

10. Cancelled.